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To:

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From:

Frank Portugal, Ph.D.

Date:

January 30, 2001

Pages

(including cover);

9

Message:

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Frank Portugal, Ph.D. Application # 09/027,089



PATENT Attorncy Docket: CAB-00

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re application of:

Frank Portugal

Appl. No.: 09/027,089

Filed: February 02, 1998

Method for Identifying Species of Shigella and E. coli Using Operon

Sequence Analysis

Art Unit:

Examiner: J. Souaya

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Commissioner for Patents

Washington, D.C. 20231,

On January 30, 2001

signed: Frank Portugal

Appeal and Continuation

Box AF

Commissioner for Patents Washington DC 20231

Sir:

In response to the Final Office Action (Paper No. 12), applicant submits the following supplemental remarks, which place the application in condition for allowance. A Notice of Appeal was filed January 16, 20001.

Supplemental Remarks

A. New Document Sabat, et. al. Proves the New Claims are Unobvious

In the previous Remarks submitted on January 22, 2001, the Applicant referred to the use of polymerase chain reaction (PCR) method of Sabat et. al. as proof that the new claims are



Application No. 09/027,089 Attorney Docket No.: CAB-001

unobvious. The Amended claims of January 22, 2001 are intended to cover any process, such as hybridization or PCR, for which an oligonucleotide is selected and used to make discriminations between or among species. In both PCR and hybridization, for example, an oligonucleotide is annealed to a complementary nucleic acid strand as dictated by Chargaff's rules on nucleic acid complementation. These rules specify that a G will hydrogen bond with a C, its complement, and that an A will hydrogen bond with its complement, which can be either a T (DNA) or U (RNA).

The optimal temperature for annealing in both PCR and hybridization reactions is dictated by the melting temperature of the duplex (T_m) formed. Once an optimal temperature is determined, in either PCR or hybridization, the oligonucleotide is annealed to its complementary template. Knowledge of an optimal temperature relative to the T_m is also used to complete each process. For PCR, that involves deliberately exceeding the optimal temperature so that the two strands of the newly formed duplex are fully and completely separated. For hybridization, the use of an optimal temperature relative to the T_m assures the complete separation of those duplexes that do not meet the preset complementary match criteria.

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Application No. 09/027,089 Attorney Docket No.: CAB-001

B. The Reference Cited by the Examiner

In the remarks to Examiner filed on January 22, 2001, regarding the citation of Hammond (5,374,718), the Applicant in his previous remarks mentioned (page 6) a comparison of the 16S rRNA sequences for *Chlamydia pneumoniae* (GenBank CHT16SR) and *Chlamydia psittaci* (GenBank E17341). To assist the Examiner is her review of the Reply and Amendment, the Applicant encloses both sets of sequences.

Respectfully submitted,

Date: January 30, 2001

By:

Applicant: Frank Portugal

Encis: GenBank CHT16SR

Gen Bank E17341

16S

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Structure Clear Genome

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Taxonomy

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History

Index

Limits

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Chlamydia pneumoniae 16S ri... 1: GI "174111" [GenBank]

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PubMed, Related Sequences, Taxonomy

21-SEP-1993

BCT 1554 bp CHT16SR LOCUS

pneumoniae

16S ribosomal RNA sequence

Chlamydia DEFINITION ACCESSION

L06108.1 GI:174111

VERSION

16S ribosomal RNA. KEYWORDS

Chlamydia pneumoniae (strain TW183) cDNA to rRNA.

Chlamydophila pneumoniae ORGANISM SOURCE

Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila

1 (bases 1 to 1554) REFERENCE

Gaydos, C.A., Palmer, L., Quinn, T.C., Falkow, S., Brooks, G.F. AUTHORS

Eiden, J.J.

psittaci and Chlamydia trachomatis as determined by analysis of Phylogenetic relationship of Chlamydia pneumoniae to Chlamydia TITLE

ribosomal DNA sequences

Int. J. Syst. Bacteriol. 43, 610-612 (1993) JOURNAL

93349759 MEDLINE Location/Qualifiers

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source

FEATURES

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BASE COUNT

366

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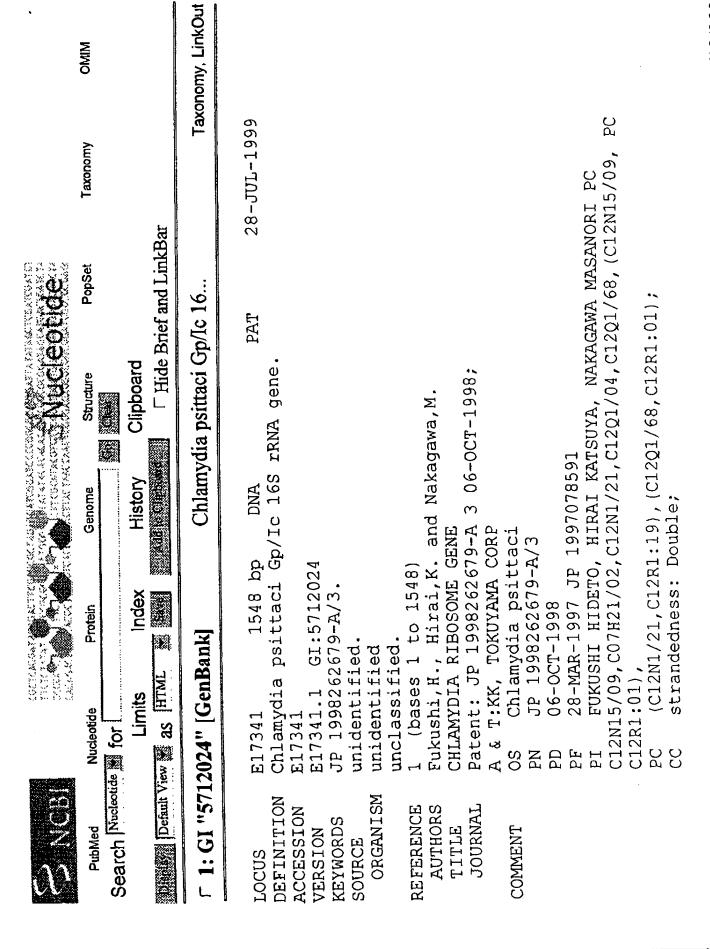
INCEL Sequence Viewer

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NCBI Sequence Viewer



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